

5620

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number:

10/519,447

Source:

PCT

Date Processed by STIC:

1-12-05

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PCT

RAW SEQUENCE LISTING

DATE: 01/12/2005

PATENT APPLICATION: US/10/519,447

TIME: 16:15:44

Input Set : A:\Q85576 Sequence Listing.txt

Output Set: N:\CRF4\01122005\J519447.raw

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3 <110> APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
4     Makoto OGINO
5     Hideki ENDOH
7 <120> TITLE OF INVENTION: METHOD FOR SCREENING AN AGENT FOR IMPROVING INSULIN
RESISTANCE
9 <130> FILE REFERENCE: Q85576
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/519,447
C--> 11 <141> CURRENT FILING DATE: 2004-12-30
11 <150> PRIOR APPLICATION NUMBER: PCT/JP03/08367
12 <151> PRIOR FILING DATE: 2003-07-01
14 <150> PRIOR APPLICATION NUMBER: JP 2002-193814
15 <151> PRIOR FILING DATE: 2002-07-02
17 <160> NUMBER OF SEQ ID NOS: 16
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1845
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (1)..(1845)
29 <223> OTHER INFORMATION:
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34 Met Ser Gly Tyr Ser Ser Asp Arg Asp Arg Gly Arg Asp Arg Gly Phe
35 1             5             10             15
37 ggt gca cct cga ttt gga gga agt agg gca ggg ccc tta tct gga aag      96
38 Gly Ala Pro Arg Phe Gly Gly Ser Arg Ala Gly Pro Leu Ser Gly Lys
39             20             25             30
41 aag ttt gga aac cct ggg gag aaa tta gtt aaa aag aag tgg aat ctt      144
42 Lys Phe Gly Asn Pro Gly Glu Lys Leu Val Lys Lys Lys Trp Asn Leu
43             35             40             45
45 gat gag ctg cct aaa ttt gag aag aat ttt tat caa gag cac cct gat      192
46 Asp Glu Leu Pro Lys Phe Glu Lys Asn Phe Tyr Gln Glu His Pro Asp
47             50             55             60
49 ttg gct agg cgc aca gca caa gag gtg gaa aca tac aga aga agc aag      240
50 Leu Ala Arg Arg Thr Ala Gln Glu Val Glu Thr Tyr Arg Arg Ser Lys
51 65             70             75             80
53 gaa att aca gtt aga ggt cac aac tgc ccg aag cca gtt cta aat ttt      288
54 Glu Ile Thr Val Arg Gly His Asn Cys Pro Lys Pro Val Leu Asn Phe
55             85             90             95
57 tat gaa gcc aat ttc cct gca aat gtc atg gat gtt att gca aga cag      336
58 Tyr Glu Ala Asn Phe Pro Ala Asn Val Met Asp Val Ile Ala Arg Gln
59             100            105            110

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61	aat ttc act gaa ccc act gct att caa gct cag gga tgg cca gtt gct	384
62	Asn Phe Thr Glu Pro Thr Ala Ile Gln Ala Gln Gly Trp Pro Val Ala	---
63	115 120 125	
65	cta agt gga ttg gat atg gtt gga gtg gca cag act gga tct ggg aaa	432
66	Leu Ser Gly Leu Asp Met Val Gly Val Ala Gln Thr Gly Ser Gly Lys	
67	130 135 140	
69	aca ttg tct tat ttg ctt cct gcc att gtc cac atc aat cat cag cca	480
70	Thr Leu Ser Tyr Leu Leu Pro Ala Ile Val His Ile Asn His Gln Pro	
71	145 150 155 160	
73	ttc cta gag aga ggc gat ggg cct att tgt ttg gtg ctg gca cca act	528
74	Phe Leu Glu Arg Gly Asp Gly Pro Ile Cys Leu Val Leu Ala Pro Thr	
75	165 170 175	
77	cgg gaa ctg gcc caa cag gtg cag caa gta gct gct gaa tat tgt aga	576
78	Arg Glu Leu Ala Gln Gln Val Gln Val Ala Ala Glu Tyr Cys Arg	
79	180 185 190	
81	gca tgt cgc ttg aag tct act tgt atc tac ggt ggt gct cct aag gga	624
82	Ala Cys Arg Leu Lys Ser Thr Cys Ile Tyr Gly Gly Ala Pro Lys Gly	
83	195 200 205	
85	cca caa ata cgt gat ttg gag aga ggt gtg gaa atc tgt att gca aca	672
86	Pro Gln Ile Arg Asp Leu Glu Arg Gly Val Glu Ile Cys Ile Ala Thr	
87	210 215 220	
89	cct gga aga ctg att gac ttt tta gag tgt gga aaa acc aat ctg aga	720
90	Pro Gly Arg Leu Ile Asp Phe Leu Glu Cys Gly Lys Thr Asn Leu Arg	
91	225 230 235 240	
93	aga aca acc tac ctt gtc ctt gat gaa gca gat aga atg ctt gat atg	768
94	Arg Thr Thr Tyr Leu Val Leu Asp Glu Ala Asp Arg Met Leu Asp Met	
95	245 250 255	
97	ggc ttt gaa ccc caa ata agg aag att gtg gat caa ata aga cct gat	816
98	Gly Phe Glu Pro Gln Ile Arg Lys Ile Val Asp Gln Ile Arg Pro Asp	
99	260 265 270	
101	agg caa act cta atg tgg agt gcg act tgg cca aaa gaa gta aga cag	864
102	Arg Gln Thr Leu Met Trp Ser Ala Thr Trp Pro Lys Glu Val Arg Gln	
103	275 280 285	
105	ctt gct gaa gat ttc ctg aaa gac tat att cat ata aac att ggt gca	912
106	Leu Ala Glu Asp Phe Leu Lys Asp Tyr Ile His Ile Asn Ile Gly Ala	
107	290 295 300	
109	ctt gaa ctg agt gca aac cac aac att ctt cag att gtg gat gtg tgt	960
110	Leu Glu Leu Ser Ala Asn His Asn Ile Leu Gln Ile Val Asp Val Cys	
111	305 310 315 320	
113	cat gac gta gaa aag gat gaa aaa ctt att cgt cta atg gaa gag atc	1008
114	His Asp Val Glu Lys Asp Glu Lys Leu Ile Arg Leu Met Glu Glu Ile	
115	325 330 335	
117	atg agt gag aag gag aat aaa acc att gtt ttt gtg gaa acc aaa aga	1056
118	Met Ser Glu Lys Glu Asn Lys Thr Ile Val Phe Val Glu Thr Lys Arg	
119	340 345 350	
121	aga tgt gat gag ctt acc aga aaa atg agg aga gat ggg tgg cct gcc	1104
122	Arg Cys Asp Glu Leu Thr Arg Lys Met Arg Arg Asp Gly Trp Pro Ala	
123	355 360 365	
125	atg ggt atc cat ggt gac aag agt caa caa gag cgt gac tgg gtt cta	1152

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126 Met Gly Ile His Gly Asp Lys Ser Gln Gln Glu Arg Asp Trp Val Leu
127      370      375      380
129 aat gaa ttc aaa cat gga aaa gct cct att ctg att gct aca gat gtg 1200
130 Asn Glu Phe Lys His Gly Lys Ala Pro Ile Leu Ile Ala Thr Asp Val
131 385      390      395      400
133 gcc tcc aga ggg cta gat gtg gaa gat gtg aaa ttt gtc atc aat tat 1248
134 Ala Ser Arg Gly Leu Asp Val Glu Asp Val Lys Phe Val Ile Asn Tyr
135      405      410      415
137 gac tac cct aac tcc tca gag gat tat att cat cga att gga aga act 1296
138 Asp Tyr Pro Asn Ser Ser Glu Asp Tyr Ile His Arg Ile Gly Arg Thr
139      420      425      430
141 gct cgc agt acc aaa aca ggc aca gca tac act ttc ttt aca cct aat 1344
142 Ala Arg Ser Thr Lys Thr Gly Thr Ala Tyr Thr Phe Phe Thr Pro Asn
143      435      440      445
145 aac ata aag caa gtg agc gac ctt atc tct gtg ctt cgt gaa gct aat 1392
146 Asn Ile Lys Gln Val Ser Asp Leu Ile Ser Val Leu Arg Glu Ala Asn
147      450      455      460
149 caa gca att aat ccc aag ttg ctt cag ttg gtc gaa gac aga ggt tca 1440
150 Gln Ala Ile Asn Pro Lys Leu Leu Gln Leu Val Glu Asp Arg Gly Ser
151 465      470      475      480
153 ggt cgt tcc agg ggt aga gga ggc atg aag gat gac cgt cgg gac aga 1488
154 Gly Arg Ser Arg Gly Arg Gly Gly Met Lys Asp Asp Arg Arg Asp Arg
155      485      490      495
157 tac tct gcg ggc aaa agg ggt gga ttt aat acc ttt aga gac agg gaa 1536
158 Tyr Ser Ala Gly Lys Arg Gly Gly Phe Asn Thr Phe Arg Asp Arg Glu
159      500      505      510
161 aat tat gac aga ggt tac tct agc ctg ctt aaa aga gat ttt ggg gca 1584
162 Asn Tyr Asp Arg Gly Tyr Ser Ser Leu Leu Lys Arg Asp Phe Gly Ala
163      515      520      525
165 aaa act cag aat ggt gtt tac agt gct gca aat tac acc aat ggg agc 1632
166 Lys Thr Gln Asn Gly Val Tyr Ser Ala Ala Asn Tyr Thr Asn Gly Ser
167      530      535      540
169 ttt gga agt aat ttt gtg tct gct ggt ata cag acc agt ttt agg act 1680
170 Phe Gly Ser Asn Phe Val Ser Ala Gly Ile Gln Thr Ser Phe Arg Thr
171 545      550      555      560
173 ggt aat cca aca ggg act tac cag aat ggt tat gat agc act cag caa 1728
174 Gly Asn Pro Thr Gly Thr Tyr Gln Asn Gly Tyr Asp Ser Thr Gln Gln
175      565      570      575
177 tac gga agt aat gtt cca aat atg cac aat ggt atg aac caa cag gca 1776
178 Tyr Gly Ser Asn Val Pro Asn Met His Asn Gly Met Asn Gln Gln Ala
179      580      585      590
181 tat gca tat cct gct act gca gct gca cct atg att ggt tat cca atg 1824
182 Tyr Ala Tyr Pro Ala Thr Ala Ala Ala Pro Met Ile Gly Tyr Pro Met
183      595      600      605
185 cca aca gga tat tcc caa taa 1845
186 Pro Thr Gly Tyr Ser Gln
187      610
190 <210> SEQ ID NO: 2
191 <211> LENGTH: 614

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192 <212> TYPE: PRT
193 <213> ORGANISM: Homo sapiens
195 <400> SEQUENCE: 2
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201 Gly Ala Pro Arg Phe Gly Gly Ser Arg Ala Gly Pro Leu Ser Gly Lys
202 20 25 30
205 Lys Phe Gly Asn Pro Gly Glu Lys Leu Val Lys Lys Lys Trp Asn Leu
206 35 40 45
209 Asp Glu Leu Pro Lys Phe Glu Lys Asn Phe Tyr Gln Glu His Pro Asp
210 50 55 60
213 Leu Ala Arg Arg Thr Ala Gln Glu Val Glu Thr Tyr Arg Arg Ser Lys
214 65 70 75 80
217 Glu Ile Thr Val Arg Gly His Asn Cys Pro Lys Pro Val Leu Asn Phe
218 85 90 95
221 Tyr Glu Ala Asn Phe Pro Ala Asn Val Met Asp Val Ile Ala Arg Gln
222 100 105 110
225 Asn Phe Thr Glu Pro Thr Ala Ile Gln Ala Gln Gly Trp Pro Val Ala
226 115 120 125
229 Leu Ser Gly Leu Asp Met Val Gly Val Ala Gln Thr Gly Ser Gly Lys
230 130 135 140
233 Thr Leu Ser Tyr Leu Leu Pro Ala Ile Val His Ile Asn His Gln Pro
234 145 150 155 160
237 Phe Leu Glu Arg Gly Asp Gly Pro Ile Cys Leu Val Leu Ala Pro Thr
238 165 170 175
241 Arg Glu Leu Ala Gln Gln Val Gln Gln Val Ala Ala Glu Tyr Cys Arg
242 180 185 190
245 Ala Cys Arg Leu Lys Ser Thr Cys Ile Tyr Gly Gly Ala Pro Lys Gly
246 195 200 205
249 Pro Gln Ile Arg Asp Leu Glu Arg Gly Val Glu Ile Cys Ile Ala Thr
250 210 215 220
253 Pro Gly Arg Leu Ile Asp Phe Leu Glu Cys Gly Lys Thr Asn Leu Arg
254 225 230 235 240
257 Arg Thr Thr Tyr Leu Val Leu Asp Glu Ala Asp Arg Met Leu Asp Met
258 245 250 255
261 Gly Phe Glu Pro Gln Ile Arg Lys Ile Val Asp Gln Ile Arg Pro Asp
262 260 265 270
265 Arg Gln Thr Leu Met Trp Ser Ala Thr Trp Pro Lys Glu Val Arg Gln
266 275 280 285
269 Leu Ala Glu Asp Phe Leu Lys Asp Tyr Ile His Ile Asn Ile Gly Ala
270 290 295 300
273 Leu Glu Leu Ser Ala Asn His Asn Ile Leu Gln Ile Val Asp Val Cys
274 305 310 315 320
277 His Asp Val Glu Lys Asp Glu Lys Leu Ile Arg Leu Met Glu Glu Ile
278 325 330 335
281 Met Ser Glu Lys Glu Asn Lys Thr Ile Val Phe Val Glu Thr Lys Arg
282 340 345 350
285 Arg Cys Asp Glu Leu Thr Arg Lys Met Arg Arg Asp Gly Trp Pro Ala
286 355 360 365

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289 Met Gly Ile His Gly Asp Lys Ser Gln Gln Glu Arg Asp Trp Val Leu
290      370      375      380
293 Asn Glu Phe Lys His Gly Lys Ala Pro Ile Leu Ile Ala Thr Asp Val
294 385      390      395      400
297 Ala Ser Arg Gly Leu Asp Val Glu Asp Val Lys Phe Val Ile Asn Tyr
298      405      410      415
301 Asp Tyr Pro Asn Ser Ser Glu Asp Tyr Ile His Arg Ile Gly Arg Thr
302      420      425      430
305 Ala Arg Ser Thr Lys Thr Gly Thr Ala Tyr Thr Phe Phe Thr Pro Asn
306      435      440      445
309 Asn Ile Lys Gln Val Ser Asp Leu Ile Ser Val Leu Arg Glu Ala Asn
310      450      455      460
313 Gln Ala Ile Asn Pro Lys Leu Leu Gln Leu Val Glu Asp Arg Gly Ser
314 465      470      475      480
317 Gly Arg Ser Arg Gly Arg Gly Gly Met Lys Asp Asp Arg Arg Asp Arg
318      485      490      495
321 Tyr Ser Ala Gly Lys Arg Gly Gly Phe Asn Thr Phe Arg Asp Arg Glu
322      500      505      510
325 Asn Tyr Asp Arg Gly Tyr Ser Ser Leu Leu Lys Arg Asp Phe Gly Ala
326      515      520      525
329 Lys Thr Gln Asn Gly Val Tyr Ser Ala Ala Asn Tyr Thr Asn Gly Ser
330      530      535      540
333 Phe Gly Ser Asn Phe Val Ser Ala Gly Ile Gln Thr Ser Phe Arg Thr
334 545      550      555      560
337 Gly Asn Pro Thr Gly Thr Tyr Gln Asn Gly Tyr Asp Ser Thr Gln Gln
338      565      570      575
341 Tyr Gly Ser Asn Val Pro Asn Met His Asn Gly Met Asn Gln Gln Ala
342      580      585      590
345 Tyr Ala Tyr Pro Ala Thr Ala Ala Pro Met Ile Gly Tyr Pro Met
346      595      600      605
349 Pro Thr Gly Tyr Ser Gln
350      610

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353 <210> SEQ ID NO: 3

354 <211> LENGTH: 1518

355 <212> TYPE: DNA

356 <213> ORGANISM: Homo sapiens

358 <220> FEATURE:

359 <221> NAME/KEY: CDS

360 <222> LOCATION: (1)..(1518)

361 <223> OTHER INFORMATION:

W--> 363 <400> 3

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364 atg ggt gaa act ctg gga gat tct cct att gac cca gaa agc gat tcc      48
365 Met Gly Glu Thr Leu Gly Asp Ser Pro Ile Asp Pro Glu Ser Asp Ser
366 1      5      10      15
368 ttc act gat aca ctg tct gca aac ata tca caa gaa atg acc atg gtt      96
369 Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Met Thr Met Val
370      20      25      30
372 gac aca gag atg cca ttc tgg ccc acc aac ttt ggg atc agc tcc gtg      144
373 Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val

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VERIFICATION SUMMARY

DATE: 01/12/2005

PATENT APPLICATION: US/10/519,447

TIME: 16:15:45

Input Set : A:\Q85576 Sequence Listing.txt

Output Set: N:\CRF4\01122005\J519447.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:32 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:29

L:363 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:361

L:638 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:636